

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant: ELLIOTT et al.
Title: KINASES AND PHOSPHATASES
Appn. No.: 10/554,917
Filing Date: 04/27/2007
Examiner: Unassigned
Art Unit: 1652
Conf. No.: 9780

TRANSMITTAL OF RESPONSE TO NOTICE TO COMPLY

Mail Stop SEQUENCE
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures, mailed February 26, 2009, in the above-identified application, transmitted herewith are the following documents:

Enclosed are:

- Return Copy of Notice to Comply including error pages (12 page).
- Statement to Support Filing and Submission in accordance with 37 C.F.R. §§1.821-1.825 (1 page).
- Sequence Listing (181 pages).
- Computer Readable Format (1 Compact disk).
- Amendment in Response to Notice Under 37 CFR §§ 1.821-825 (4 pages).

The Commissioner is hereby authorized to charge any fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by the credit card payment form being unsigned, providing incorrect information resulting in a rejected credit card transaction, or even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741.

Please direct all correspondence to the undersigned attorney or agent at the address indicated below.

Respectfully submitted,

By Michele M. Simkin

Date: March 24, 2009

FOLEY & LARDNER LLP
Customer Number: 22428
Telephone: (202) 672-5538
Facsimile: (202) 672-5399

Michele M. Simkin
Attorney for Applicant
Registration No. 34,717



Notice to Comply

Application No.
10554917

Applicant(s)
ELLIOTT ET AL.

Examiner
SHERIDAN SWOPE

Art Unit
1652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 11114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other:

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment specifically directing its entry into the application.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-0731 or (571) 272-0951

For CRF Submission Help, call (571) 272-2510

PatentIn Software Program Support

Technical Assistance 1-866-217-9197 or 703-305-3028 or 571-272-6845

PatentIn Software is Available At www.USPTO.gov

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

/SHERIDAN SWOPE/
Primary Examiner, Art Unit 1652



=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=15; hr=12; min=18; sec=18; ms=279;]

=====

Reviewer Comments:

<400> 3

Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile
1 5 10 15

Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln

20

25

30

Please remove the blank line between the amino acids and their respective numbers above. This error appears in subsequent amino acid sequences. Also, please remove the blank lines between rows of nucleotides (this appears in subsequent sequences).

(end of Sequence 86)

ttttatTTTA tttatTTTt gatggagtct tgcactccag cctggtgaca gact

1914

PF-1506 PCT

1/94

WASH_1695548.1

Please remove the above three lines of text, which appear at the end of the submitted file.

Application No: 10554917

Version No: 1.0

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (13)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (15)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)

Input Set:

Output Set:

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Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
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E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
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E 355	Empty lines found between the amino acid numbering and the
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E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31) POS (915)
E 330	Invalid protein , found in SEQID(86) POS (1) Invalid Protein:PCT

Input Set:

Output Set:

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Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 112	Upper case found in data; Found at position(1914) SeqId(86)
W 112	Upper case found in data; Found at position(1915) SeqId(86)
W 112	Upper case found in data; Found at position(1916) SeqId(86)
W 112	Upper case found in data; Found at position(1917) SeqId(86)
E 259	Found undefined lettercode; POS (1919) SEQID(86)
E 259	Found undefined lettercode; POS (1920) SEQID(86)
E 259	Found undefined lettercode; POS (1921) SEQID(86)
E 259	Found undefined lettercode; POS (1922) SEQID(86)
E 259	Found undefined lettercode; POS (1923) SEQID(86)
E 259	Found undefined lettercode; POS (1924) SEQID(86)
E 259	Found undefined lettercode; POS (1925) SEQID(86)
E 259	Found undefined lettercode; POS (1926) SEQID(86)
E 259	Found undefined lettercode; POS (1927) SEQID(86)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 1927 SEQID(86)
E 253	The number of bases differs from <211> Input: 1914 Calculated:1927 SEQID (86)

<110> INCYTE CORPORATION; ELLIOTT, Vicki S.;
KHARE, Reena; RICHARDSON, Thomas W.;
MARQUIS, Joseph P.; SWARNAKAR, Anita;
HAFALIAL, April J.A.; BECHA, Shanya D.;
CHAWLA, Narinder K.; BAUGHN, Mariah R.;
LEE, Soo Yeun; TRAN, Uyen K.;
YUE, Henry; NGUYEN, Danniel B.;
THORNTON, Michael B.; GURURAJAN, Rajagopal;
GANDHI, Ameena R.; LU, Yan;
YAO, Monique G.; LI, Joana X.;
LUO, Wen; LEE, Ernestine A.;
FORSYTHE, Ian J.; ISON, Craig H.;
WILSON, Amy D.; JIN, Pei

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<130> PF-1506 PCT

<140> 10554917

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20 25 30

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				35				40				45		
Trp	Leu	Ser	Leu	Cys	Thr	Ala	Met	Ser	Pro	Leu	Thr	Thr	Glu	Ile
				50				55				60		
Trp	Ala	Leu	Arg	Arg	Gly	Asn	Ser	Ser	Ala	Ser	Trp	Ser	Arg	Ala
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			20					25					30	
Leu	Thr	Gln	Leu	Leu	Asn	Ser	Leu	Cys	Thr	Ala	Val	Lys	Ala	Ile
			35					40					45	
Ser	Ser	Ala	Val	Arg	Lys	Ala	Gly	Ile	Ala	His	Leu	Tyr	Gly	Ile
			50					55					60	
Ala	Gly	Ser	Thr	Asn	Val	Thr	Gly	Asp	Gln	Val	Lys	Lys	Leu	Asp
			65					70					75	
Val	Leu	Ser	Asn	Asp	Leu	Val	Met	Asn	Met	Leu	Lys	Ser	Ser	Phe
			80					85					90	
Ala	Thr	Cys	Val	Leu	Val	Ser	Glu	Glu	Asp	Lys	His	Ala	Ile	Ile
			95					100					105	
Val	Glu	Pro	Glu	Lys	Arg	Gly	Lys	Tyr	Val	Val	Cys	Phe	Asp	Pro
			110					115					120	
Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp	Cys	Leu	Val	Ser	Val	Gly	Thr
			125					130					135	
Ile	Phe	Gly	Ile	Tyr	Arg	Lys	Lys	Ser	Thr	Asp	Glu	Pro	Ser	Glu
			140					145					150	
Lys	Asp	Ala	Leu	Gln	Pro	Gly	Arg	Asn	Leu	Val	Ala	Ala	Gly	Tyr
			155					160					165	
Ala	Leu	Tyr	Gly	Ser	Ala	Thr	Met	Leu	Val	Leu	Ala	Met	Asp	Cys
			170					175					180	
Gly	Val	Asn	Cys	Phe	Met	Leu	Asp	Pro	Asp	Asn	Ser	Ala	Pro	Tyr
			185					190					195	
Gly	Ala	Arg	Tyr	Val	Gly	Ser	Met	Val	Ala	Asp	Val	His	Arg	Thr
			200					205					210	
Leu	Val	Tyr	Gly	Ile	Phe	Leu	Tyr	Pro	Ala	Asn	Lys	Lys	Ser	
			215					220					225	
Pro	Asn	Gly	Lys	Leu	Arg	Leu	Leu	Tyr	Glu	Cys	Asn	Pro	Met	Ala
			230					235					240	
Tyr	Val	Met	Glu	Lys	Ala	Gly	Gly	Met	Ala	Thr	Thr	Gly	Lys	Glu
			245					250					255	
Ala	Val	Leu	Asp	Val	Ile	Pro	Thr	Asp	Ile	His	Gln	Arg	Ala	Pro
			260					265					270	
Val	Ile	Leu	Gly	Ser	Pro	Asp	Asp	Val	Leu	Glu	Phe	Leu	Lys	Val
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Arg Gly Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val
35 40 45
Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Lys Lys Leu Thr
50 55 60
Arg Tyr Leu Asn Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val
65 70 75
Gly Gln Tyr Arg Arg Asp Val Val Lys Thr Tyr Lys Ser Phe Glu
80 85 90
Phe Phe Leu Pro Asp Asn Glu Glu Gly Leu Lys Ile Arg Lys Gln
95 100 105
Cys Ala Leu Ala Ala Leu Arg Asp Val Arg Arg Phe Leu Ser Glu
110 115 120
Glu Gly Gly His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg
125 130 135
Glu Arg Arg Ala Thr Ile Phe Asn Phe Gly Glu Gln Asn Gly Tyr
140 145 150
Lys Thr Phe Phe Val Glu Ser Ile Cys Val Asp Pro Glu Val Ile
155 160 165
Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser Pro Asp Tyr Val
170 175 180
Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met Arg Arg Ile
185 190 195
Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp Leu Asp
200 205 210
Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser Tyr
215 220 225
Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
230 235 240
Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys
245 250 255
Arg His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly
260 265 270
Asp Pro Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu
275 280 285
Ala Gln Phe Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp
290 295 300
Thr Ser Gln Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly
305 310 315
Val Pro Tyr Glu Gln Trp Lys Val Leu Asn Glu Ile Asp Ala Ser

320	325	330
Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu		
335	340	345
Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met		
350	355	360
Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ala Ala Glu Gln Leu		
365	370	375
Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu Thr Pro		
380	385	390
Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Phe Leu Asn Val Ala		
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Arg Val Leu Ser Gly Asp Leu Gly Gln Leu Pro Thr Gly Ile Arg		
35	40	45
Asp Phe Val Glu His Ser Ala Arg Leu Cys Gln Pro Glu Gly Ile		
50	55	60
His Ile Cys Asp Gly Thr Glu Ala Glu Asn Thr Ala Thr Leu Thr		
65	70	75
Leu Leu Glu Gln Gln Gly Leu Ile Arg Lys Leu Pro Lys Tyr Asn		
80	85	90
Asn Cys Trp Leu Ala Arg Thr Asp Pro Lys Asp Val Ala Arg Val		
95	100	105
Glu Ser Lys Thr Val Ile Val Thr Pro Ser Gln Arg Asp Thr Val		
110	115	120
Pro Leu Pro Pro Gly Gly Ala Arg Gly Gln Leu Gly Asn Trp Met		
125	130	135
Ser Pro Ala Asp Phe Gln Arg Ala Val Asp Glu Arg Phe Pro Gly		
140	145	150
Cys Met Gln Gly Arg Thr Met Tyr Val Leu Pro Phe Ser Met Gly		
155	160	165
Pro Val Gly Ser Pro Leu Ser Arg Ile Gly Val Gln Leu Thr Asp		
170	175	180
Ser Ala Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Leu Gly		
185	190	195
Thr Pro Val Leu Gln Ala Leu Gly Asp Gly Asp Phe Val Lys Cys		
200	205	210
Leu His Ser Val Gly Gln Pro Leu Thr Gly Gln Asp Pro Gly His		
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His Gln Pro Cys Arg Glu Ala Leu Cys Gly Ser Arg Leu Pro		

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				20				25						30
Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
				35				40						45
Ile	Gly	Thr	Pro	Thr	Lys	Val	Phe	Asn	Leu	Gly	Gln	Tyr	Arg	Arg
					50			55						60
Glu	Ala	Val	Ser	Tyr	Lys	Asn	Tyr	Glu	Phe	Phe	Leu	Pro	Asp	Asn
				65				70						75
Met	Glu	Ala	Leu	Gln	Ile	Arg	Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu
				80				85						90
Lys	Asp	Val	His	Asn	Tyr	Leu	Ser	His	Glu	Glu	Gly	His	Val	Ala
				95				100						105
Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile
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Leu	Gln	Phe	Ala	Lys	Glu	His	Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu
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Ser	Ile	Cys	Asn	Asp	Pro	Gly	Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln
				140				145						150
Val	Lys	Leu	Gly	Ser	Pro	Asp	Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys
				155				160						165
Val	Leu	Glu	Asp	Phe	Leu	Lys	Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn
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His	Ala	Thr	Trp											

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Tyr	Arg	Arg	Glu	Ala	Val	Ser	Tyr	Lys	Asn	Tyr	Glu	Phe	Phe	Leu
				20				25						30

Pro Asp Asn Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu
 35 40 45
 Ala Ala Leu Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly
 50 55 60
 His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg
 65 70 75
 Ser Leu Ile Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe
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 Phe Ile Glu Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn
 95 100 105
 Ile Arg Gln Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp
 110 115 120
 Arg Glu Lys Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr
 125 130 135
 Glu Val Asn Tyr Gln Pro Leu Asp Glu Glu Leu Asp Ser His Leu
 140 145 150
 Ser Tyr Ile Lys Ile Phe Asp Val Gly Thr Arg Tyr Met Val Asn
 155 160 165
 Arg Val Gln Asp His Ile Gln Ser Arg Thr Val Tyr Tyr Leu Met
 170 175 180
 Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg His Gly
 185 190 195
 Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly Asp Ser Gly
 200 205 210
 Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala Asn Phe
 215 220 225
 Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His
 230 235 240
 Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr
 245 250 255
 Glu Gln Trp Lys Ala Leu Asn Glu Ile Asp Ala Gly Val Cys Glu
 260 265 270
 Glu Met Thr Tyr Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe
 275 280 285
 Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly
 290 295 300
 Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met
 305 310 315
 Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala
 320 325 330

Val Met Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ser Ser Asp
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 Glu Leu Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu
 350 355 360
 Thr Pro Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Tyr Leu Asn
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Tyr

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Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
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Ile	Gly	Thr	Pro	Thr	Lys	Asp	Asn	Met	Glu	Ala	Leu	Gln	Ile	Arg
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Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu	Lys	Asp	Val	His	Asn	Tyr	Leu
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Ser	His	Glu	Glu	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr
	80					85					90			
Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile	Leu	Gln	Phe	Ala	Lys	Glu	His
	95					100					105			
Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu	Ser	Ile	Cys	Asn	Asp	Pro	Gly
	110					115					120			
Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp
	125					130					135			
Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys	Val	Leu	Glu	Asp	Phe	Leu	Lys
	140					145					150			
Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn	Tyr	Gln	Pro	Leu	Asp	Glu	Glu
	155					160					165			
Leu	Asp	Ser	His	Leu	Ser	Tyr	Ile	Lys	Ile	Phe	Asp	Val	Gly	Thr
	170					175					180			
Arg	Tyr	Met	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg	Thr
	185					190					195			
Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr
	200					205					210			
Leu	Cys	Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Ile	Arg	Gly	Arg	Ile
	215					220					225			
Gly	Gly	Asp	Ser	Gly	Leu	Ser	Val	Arg	Gly	Lys	Gln	Tyr	Ala	Tyr
	230					235					240			
Ala	Leu	Ala	Asn	Phe	Ile	Gln	Ser	Gln	Gly	Ile	Ser	Ser	Leu	Lys
	245					250					255			
Val	Trp	Thr	Ser	His	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala
	260					265					270			
Leu	Gly	Val	Pro	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp
	275					280					285			
Ala	Gly	Val	Cys	Glu	Glu	Met	Thr	Tyr	Glu	Glu	Ile	Arg	Glu	His
	290					295					300			
Tyr	Pro	Glu	Glu	Phe	Ala	Leu	Arg	Asp	Gln	Asp	Lys	Tyr	Arg	Tyr
	305					310					315			
Arg	Tyr	Pro	Lys	Gly	Glu	Ser	Tyr	Glu	Asp	Leu	Val	Gln	Arg	Leu
	320					325					330			
Glu	Pro	Val	Ile	Met	Glu	Leu	Glu							